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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2003, 15:04:29 ; Search time 17.2201 Seconds  
(without alignments)  
2160.495 Million cell updates/sec

Title: US-09-807-933B-9

Perfect score: 2106

Sequence: 1 MKFTVAITSAVALALSSA.....TFKEVTCPAELTTRSGCERK 387

Scoring table: BLOSUM62

Gapop: 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.\*

1: PIR1.\*

2: PIR2.\*

3: PIR3.\*

4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	758.5	36.0	229	JC7308	cellulase (EC 3.2.1.4)
2	592	28.1	511	S10527	endoglucanase B pr
3	525.5	25.0	393	S59499	cellulase eg11 - s
4	226.5	10.8	471	A26160	cellulose 1,4-beta
5	226.5	10.8	471	A38979	cellulose 1,4-beta
6	190	9.0	418	S28372	cellulase (EC 3.2.1.4)
7	186	8.8	410	S68153	cellulase (EC 3.2.1.4)
8	182	8.6	2395	S50820	surface protein ty
9	177	8.4	475	S49886	probable membrane
10	174.5	8.3	378	S61992	SLG1 protein - yea
11	174.5	8.3	533	T33912	hypothetical prote
12	172	8.2	438	S70602	cellulose 1,4-beta
13	171.5	8.1	1428	T08852	lustrin A - Califo
14	171	8.1	1777	T34369	hypothetical prote
15	168.5	8.0	400	S61855	hypothetical prote
16	168.5	8.0	4776	E95206	cell wall surface
17	166.5	7.9	481	A35628	loricrin - mouse
18	166.5	7.9	503	S63257	probable membrane
19	166	7.9	605	T33913	hypothetical prote
20	164	7.8	937	S58135	hypally regulated
21	163	7.7	600	S07638	spore coat protein
22	163	7.7	1275	T33369	hypothetical prote
23	163	7.7	1797	T21889	hypothetical prote
24	163	7.7	1805	T21888	hypothetical prote
25	161.5	7.7	354	T46740	microfilarial shea
26	161.5	7.7	662	A45155	mucin FIM-C.1 - Af
27	160	7.6	2543	T31687	surface antigen - P
28	159.5	7.6	2718	A23475	G surface protein
29	158.5	7.5	537	B33485	spore coat protein

30	158	7.5	786	1	A47547	serine proteinase
31	158	7.5	1022	2	T34433	hypothetical prote
32	158	7.5	1367	1	S48478	glucan 1,4-alpha-g
33	158	7.5	2232	2	T34434	hypothetical prote
34	156.5	7.4	2764	2	S09118	G surface protein
35	155.5	7.4	281	2	T49537	hypothetical prote
36	153	7.3	242	2	S60143	cellulase (EC 3.2.1.4)
37	152	7.2	463	2	T38444	hypothetical prote
38	151.5	7.2	962	2	S03818	carboxymethylcellu
39	151	7.2	738	2	S40992	hypothetical prote
40	151	7.2	739	2	B88553	protein K04H4.2b I
41	151	7.2	786	2	T16509	hypothetical prote
42	151	7.2	2639	2	T31328	fibronin - Chinese
43	150	7.1	13288	2	T03099	mucin, submaxillar
44	149.5	7.1	556	2	S51892	probable membrane
45	149.5	7.1	888	2	T46726	secreted acid phos

ALIGNMENTS

RESULT 1

JC7308

Cellulase (EC 3.2.1.4) - Scopulariopsis brevicaulis

N:Alternate names: endoglucanase I

C:Species: Scopulariopsis brevicaulis

C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000

C:Accession: JC7308; PC7087

R:Nakatani, F.; Kawaguchi, T.; Takada, G.; Sumitani, J.; Moriyama, Y.; Arai, M.

Biosci. Biotechnol. Biochem. 64, 1238-1246, 2000

A:Title: Cloning and sequencing of an endoglucanase gene from Scopulariopsis brevicaulis

A:Reference number: JC7308

A:Accession: JC7308

A:Molecule type: DNA

A:Residues: 1-229 <NAK>

A:Experimental source: strain TOP-1212

A:Accession: PC7087

A:Molecule type: protein

A:Residues: 21-37;149-164 <NA2>

C:Genetics:

A:Gene: eg1

A:Introns: 147/3

C:Keywords: glycosidase; hydrolase

Query Match	36.0%	Score	758.5	DB 2	Length	229			
Best Local Similarity	62.8%	Pred. No.	7.1e-39						
Matches	130	Conservative	30	Mismatches	44	Indels	3	Gaps	3
QY	183	SGSGTTRYWDCCKASCSWPGKASVT-GPVDTCASNGISLLDAN-AOSGCN-GGNGFMCN	239						
DB	22	SGTGTTRYWDCCKSPCSWPKAPLSQGPWMTCDINDNPLDDGGLTESGCEPGGAYMCS	81						
		:       :							

RESULT 2

S10527

endoglucanase B precursor - Pseudomonas fluorescens

C:Species: Pseudomonas fluorescens

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 08-Oct-1999

C:Accession: S10527

R:Gilbert, H.J.; Hall, J.; Hazlewood, G.P.; Ferreira, L.M.A.

Mol. Microbiol. 4, 759-767, 1990

A;Title: The N-terminal region of an endoglucanase from *Pseudomonas fluorescens* subspecies  
A;Reference number: S10527; MUID:90355836; PMID:2117693

A;Accession: S10527  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-511 <GIL>  
A;Cross-references: EMBL:X52615; NID:945497; PIDN:CAA36844.1; PID:945498  
C;Superfamily: bacterial cellulose-binding domain homology; glycosidase GMDW domain hom  
F;31-128/Domain: bacterial cellulose-binding domain homology <BCB>  
F;180-217/Domain: glycosidase GMDW domain homology <GMD>  
F;32-127/Disulfide bonds: #status predicted

Query Match 28.1%; Score 592; DB 2; Length 511;  
Best Local Similarity 33.9%; Pred. No. 1.4e-28;  
Matches 147; Conservative 65; Mismatches 132; Indels 90; Gaps 17;  
QY 8 TSIAVALALSSAEEAASCSVYGO--CGGIGWTGPTCCDAGTCKA-----QKDKYYSQ 60  
DB 102 SVEFGVQNGSSRAQVPAVTGALCGGQGSAPSSVASSSSSSSVSVSTPRSSSSVS 161  
QY 61 CIPKPGSSSSSSSSSVYSSQCGIGWSG---PTC-----CEGSGTCVAQEGNKYYSQ 109  
DB 162 SVP---GTSSSSS--SSVLTGAQCNWYGLTPLCMTNTSGWYEDGRSCVAR-----TT 211  
QY 110 CLPGSHSNAGNASTTKTSTTTAKATATVTKVTKTKTKTKTKTKTKTKTKTKTKTK 169  
DB 212 C--SAQAPYGVIVSTSSSTPLSSSSSSSSVA-----SSSLSSATSSSA 254  
QY 170 SSSAGYKVSIGKSGSGSTRYWDCCCKASCWPGKA--SVTGPVDFTCASNGISLLDANAQS 228  
DB 255 SSVSSVPIIDGG--CNGVATRWDCCKPHGWSANVPSLVPLQSCSANTRLSQVSGS 312  
QY 229 GCGNGGFMCMNNQWAVNDELAYGFAAASLAGSNEAGWCCG--CYELTFT----- 277  
DB 313 SCGGGGYMCWKIPFVAVSPTLAYAATS-----SGDVGRCYQLQFTGSSYNAPGDP 366  
QY 278 -SGAASGKQVQVQVNTGDLGNSHFDLQMPGGVGIFNGCAQWGAQWAPNDGARYGV- 335  
DB 367 GSAALAGKTMVQATNIGYDVSGGQFDILVPGGGVGAFNACSAQWGVNSELGAQYGGFL 426  
QY 336 -----SVSPD-----CASL-----PSALQAGCKWRFNWFKNSDNPTWTFKEV 372  
DB 427 AACKQOLGVNASLSQVSKVLCNRCDSVFGSRGLTQLOQCTWFAEFADNPGLKYKEV 486  
QY 373 TCPAELTTRSGGER 386  
DB 487 PCPAELTTRSGMNR 500

RESULT 3  
S59499  
cellulase egII - smut fungus (Ustilago maydis)  
C;Species: Ustilago maydis (corn smut)  
C;Date: 20-Jul-1996 #sequence\_revision 13-Mar-1997 #text\_change 28-May-1999  
C;Accession: S59499  
R;Schauwecker, F.; Wanner, G.; Kahmann, R.  
Biol. Chem. Hoppe-Seyler 376, 617-625, 1995  
A;Title: Filament-specific expression of a cellulase gene in the dimorphic fungus *Ustilago*  
A;Reference number: S59499; MUID:96145728; PMID:8590631  
A;Accession: S59499  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-393 <SCH>  
A;Cross-references: GB:S81598; NID:g1478378; PIDN:AAB36147.1; PID:g1478379

Query Match 25.0%; Score 525.5; DB 2; Length 393;  
Best Local Similarity 48.6%; Pred. No. 1.1e-24;  
Matches 107; Conservative 28; Mismatches 60; Indels 25; Gaps 10;  
QY 185 SGTSTRYWDCCASCWPGKASVTPGVDTCAASNGISLLDA-----NAQSCGNGGNGFMCMN 240  
DB 26 AGVATRWDCCLASAWESKAPVYAVDACKADGVTLIDSKDPSQSCGNGGNGFMCMSC 85

QY 241 NOPWAVNDE-----LAYFAAASLAGSNEAGWCCGCGCYELTFTSGAASGK-----KMVQVVT 291  
DB 86 MQPF--DDETDPTLAFPGA--FTTQESDITDCACFYAEFHD-AQGWAKRNKLIQVVT 140  
QY 292 NTGGDLGNSHFDLQMPGGVGIF-NGCAQWGAQWAPNDGARYGVSSVSDCASLPSALQA 350  
DB 141 NVGQDVQSQNFDFQIFGGGLGAPKCPQAPQWGVSEALMGDOYGVKASATECSKLPKPLQE 200  
QY 351 GCKWRFN-WPKNSDNPTM--TFKEVTCPAELTTRSGCERK 387  
DB 201 GCKWRFEW---GDNVPLKGSPPKRVKCPKSLIDRSGCQRK 237

## RESULT 4

A26160  
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (*Trichoderma reesei*)  
N;Alternate names: exo-cellobiohydrolase II  
C;Species: *Trichoderma reesei*  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A26160; A26472  
R;Chen, C.M.; Gritzali, M.; Stafford, D.W.  
Bio/Technology 5, 274-278, 1987  
A;Title: Nucleotide sequence and deduced primary structure of cellobiohydrolase II from  
A;Reference number: A26160  
A;Accession: A26160  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-471 <CHE>  
R;Teeri, T.T.; Lehtovaara, P.; Kauppinen, S.; Salovuori, I.; Knowles, J.  
Gene 51, 43-52, 1987  
A;Title: Homologous domains in *Trichoderma reesei* cellulolytic enzymes: gene sequence an  
A;Reference number: A26472; MUID:87248061; PMID:3596237  
A;Accession: A26472  
A;Molecule type: DNA  
A;Residues: 1-471 <TEE>  
A;Cross-references: GB:M16190; NID:g170540; PIDN:AAA34210.1; PID:g170541  
C;Genetics:  
A;Introns: 31/2; 160/2; 243/1  
C;Superfamily: cellulose 1,4-beta-cellobiosidase II; fungal cellulose-binding domain hom  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation  
F;31-62/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 10.8%; Score 226.5; DB 1; Length 471;  
Best Local Similarity 25.1%; Pred. No. 1.1e-06;  
Matches 125; Conservative 37; Mismatches 145; Indels 191; Gaps 30;

QY 7 ITSIAVALALSSSA---EAAACSSVYQCGGIGWTGPTCCDAGTCKAOKDKNKYYSQICP 63  
DB 6 LTTLATLATLAASVPLEERQACSSVWQCGQWNGSGPTCCASGTCVYSND--YYSQCLP 63  
QY 64 KPGSSSSSSSSSVYSSQCGGIGWSGPTCCES-----GSTCVAQEGNKY 106  
DB 64 GAASSSSSSTRAASTSRV-----SPTTSRSSSATPPPGSTTRVPVPGSGTATYSGNPF 117  
QY 107 YSQCLPGSHSNAGNASTTKTS-TKSTTTAKATATVTKVTKTKTKTKTKTKTKTSTTAA 165  
DB 118 VG-VTPWANYAYSEVSSLAIPSLTGAMATAAAAVAKVPFPMWLDLTKPLMEQTLADI 176  
QY 166 STSTSSSAGYKVISGGKSGSGSTTRY---WDCC-----KASCSWPGKASVTPGVDTCA 215  
DB 177 RTANKNGNY-----AQQFVVYDLPDRDCAALASNGEYSIADGGVAKYKNYIDTIR 227  
QY 216 SNGISLLD-----ANAQSCGNGGNGFMCMN-----NOP-- 243  
DB 228 QIVVEYSIDIRLLVIEPDSLNLNLVNLGTPKCANQAQAY-----LEGINYAVTQNLNPNV 282  
QY 244 -----WAVN-DELAIFYA-----AASIAGSNEAGWCCGCGYEL 274  
DB 283 AMYLDAGHAGWLPANQDPAALFANVKNASSPRALRLGLATNVANYN--GW-----NI 335  
QY 275 T-----FTSG--AASGKMWVQVNTGDLGNSH-----FDL-----QMPGGVGIFNGC 317  
DB 336 TSPSPSYTQGNVAVNEKLYIHAI---GPLLANHGWNSAFFITDQGRSQKPTG----- 384



[illegible]

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Qy 178 ISGKSG-SGSTTRYD-----CCX-----ASCWPGKASVTPGVDTCASNGISLLDAN 225
Db 204 IYGLDAFPGSEKFDQGTIPCDKPPSGQGVISIDWIGEGWGVENTDTSTGGSCKEKS 263
Qy 226 AQS-CCNGG-----NGFCMNNQPNVNDLAY-----GFAAASAG-- 261
Db 264 YCSYSCQPGMSKTOWPSPQSDGRSVGLLCKNGLYRSNTDADYLCWGWVEAAYVWSKL 323
Qy 262 SNEAGWCCGCE-----LFTSTGAASCKKMWVQ-----VNTTGGDLGSHFDLQMPGG 310
Db 324 SKGVAICETDYPGTENMVIPFVEGGSLPLTVVDODTYFTWEGKKTSAQYY---VNNAG 380
Qy 311 VGIFNGCAQWGPNDGNG-----ARYGVSSVS 339
Db 381 VSVEDGCI--WGTSGSGIGNWAPLNFAGAGTGGVTVLS 416

RESULT 10
S61992
SLG1 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein Q2545; protein UNE378; protein YOR008c
C:Species: Saccharomyces cerevisiae
C:Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 21-Jul-2000
C:Accession: S61992; S66873; S72141
R:Sterky, F.; Uhlen, M.
A:Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharo
A:Reference number: S72141
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-378 <STB>
A:Cross-references: EMBL:U43491; NID:g1150992; PID:g1151004
R:Petersson, B.; Sterky, F.; Uhlen, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66882
A:Accession: S66873
A:Molecule type: DNA
A:Residues: 1-378 <PET>
A:Cross-references: EMBL:Z74916; NID:g1420101; PID:g252318; PID:g1420102; MIPS:YOR008c
A:Experimental source: strain S288C
R:Sterky, F.; Holmberg, A.; Petersson, B.; Uhlen, M.
Yeast 12, 1091-1095, 1996
A:Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from Saccharo
A:Reference number: S72130; MUID:97051599; PMID:8896276
A:Accession: S72141
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-378 <STW>
A:Cross-references: EMBL:U43491; NID:g1150992; PID:AAC49488.1; PID:g1151004
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C:Genetics:
A:Gene: SGD:SLG1
A:Cross-references: SGD:S0005534; MIPS:YOR008c
A:Map position: 15R
C:Keywords: transmembrane protein
P:270-286/Domain: transmembrane #status predicted <TMM>

Query Match 8.3%; Score 174.5; DB 2; Length 378;
Best Local Similarity 25.8%; Pred. No. 0.0012;
Matches 85; Conservative 48; Mismatches 112; Indels 85; Gaps 16;

Qy 8 TSIAYA-LALSSAEA-----ASCSSVYGGCGGIGTGTCTCDAGSTCKAQNKY-- 57
Db 6 TSLLLALLSILSQANAYEVNCFSLPDPFSKADSYNNQSSHCN--SECSAKGASYAL 63
Qy 58 --YSQCI---PKPKGSSSSSSCSVYSGGIGWSPGPTCCSGSGSTCVAGQGNKYVQCLP 112
Db 64 YNHSEYCGDTPNPSSESTSSCNTY--C--FGYSSEMCGGEDAYSVTQLDSDTNSNIS 119
Qy 113 GSHSNNAGNASTKTKSTTTAKATATV--TTKTVTKTKTKTKSTTTAASTGTS 170
Db 120 SDDSTESTASSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 179
Qy 171 SSAGYKVI-SGGKSGSGSTTRYWDCCKASCSWPGKASVTPGVDTCASNGISLLDANAQS-- 228
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Db 180 QS-----SSTVTSSSLTS--DTLATSSSSQSDATSI 212
Qy 229 -----GCNGGNG-FWCNNQPNVNDLAYGFAAASAGSNEAGWCCCGCYELTFTSGAAS 282
Db 213 YSTTFHTEGGSTIEFTVNTITASAQNSGATG-----TAGSDS-----TSGSKT 255
Qy 283 GKMWVQVVTNTEGDLGSHFDLQMPGGVG 312
Db 256 HKKK-----ANVGAIVGG-----VVGGVVG 275

RESULT 11
T33912
hypothetical protein Y25C1A.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33912
R:Kalicki, J.; Smith, A.; Gibson, A.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y25C1A.
A:Reference number: Z21437
A:Accession: T33912
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-533 <KAL>
A:Cross-references: EMBL:AF125459; PIDN:AAD12832.1; GSPDB:GN00020; CBSP:Y25C1A.4
A:Experimental source: strain Bristol N2; clone Y25C1A
C:Genetics:
A:Gene: CBSP:Y25C1A.4
A:Map position: 2
A:Introns: 25/3; 170/3; 241/1; 378/3; 415/1

Query Match 8.3%; Score 174.5; DB 2; Length 533;
Best Local Similarity 26.2%; Pred. No. 0.0016;
Matches 77; Conservative 43; Mismatches 103; Indels 71; Gaps 12;

Qy 121 NASSTKTKSTKSTTTAKATATVTTKTKTKTKTKTKTKTTTAAASTSTSSAGYKVISG 180
Db 18 NSWAQDPTTATSTTTVPSTSTVTTTVAISSGSTT-ASTAAGGSTST-TAAGGSTAST 75
Qy 181 KSGSGSTTRYWDCCKASCSWPGKASVTPGVDTCASNGISLLDANAQSGCNGGFMCNN 240
Db 76 AAGGSTSTT-----AAGGSTASTAAGGPTGTAAAGGSTASTA----- 112
Qy 241 NQPNVNDLAYGFAAASAGSNEAGWCCCGCYELTFTSGAASGKMWVQVNTTGGDLGSH 300
Db 113 -----AGGSTASTAAGGSTASTVAGATSVVPSSPAPPTOPPV-----NNGCELGMK 158
Qy 301 HFDLQMPGGG--VGIFNG-CAAQWGPNDGNGARYGVSSVSDCASLPSALQAGKWR-- 355
Db 159 PFN--RPSGGWCIVKFPGYFALKEHAEN---ACQANGAATLTGLONKAEALFIOCEYRNS 213
Qy 356 -----FNWFKN-----SDNPTMTFTKVTCPAELTTRSG-----CERK 387
Db 214 PYFSCFCFQNSVLGYCSSTVEVLYEYSSMLSEMSAPSGSVWIGIHRTPCNRK 267

RESULT 12
S70602
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - cultivated mushroom
N:Alternate names: cellulase
C:Species: Agaricus bisporus (cultivated mushroom)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S70602
R:Yaguee, E.; Chow, C.M.; Challen, M.P.; Thurston, C.F.
Curr. Genet. 30, 56-61, 1995
A:Title: Correlation of exons with functional domains and folding regions in a cellulase
A:Reference number: S70602; MUID:96269930; PMID:8662210
A:Accession: S70602
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <YAG>
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[illegible]



A;Map position: 1

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Query Match      8.0%; Score 168.5; DB 2; Length 402;
Best Local Similarity 27.8%; Pred. No. 0.0029;
Matches 84; Conservative 27; Mismatches 132; Indels 59; Gaps 12;

Qy 41 TCCDAGSTCKAOKNKYYSQCIPKPGSSSSSSCSVYQCGGIGWGG-PTCCESGSTCV 99
Db 9 TASAAGTLTRASTYPNTYNSNPADASSMPSTWTTVPQTSSSSTSTTTATSSSGTT 68

Qy 100 AQEGNKYYSQLPGS--HSNNAGNASSTKKT-----STKST-----TTAK 138
Db 69 AESSSTKSAATMSGSTTHTTSSATASSTASTSTSSYSTSYSTSTKTTTGTGISTTAS 128

Qy 139 ATATVTTKTVTK-----TTTKTTTKT-----STTAAASTSTSSAGYKVIS---CGK 182
Db 129 AAPTSTASTSTSSYSTSYSTSTKTTTGTGTTASAAPTSTSTANSASSTNPS 188

Qy 183 SGSGSTTRYWDCKKASCSWP-GKASVTGPDVTC--SNG-----ISLLDANAQGCNGN 234
Db 189 SGSKPTAMTGTTANTSPSAPTSSPSTTNSSTAAVTSSGSKPTTTRTTANTSSASTSS 248

Qy 235 GFMCNNOPWAVNDELAYGFAAASIAGSNE---AGWCCGCYELTFTGAASGKKMNVQVT 291
Db 249 ASPTNSSTSTPTN-----SSAGSKPTMTGTTTNTSTSTTTSSASTTKSSSSAT 298

Qy 292 NT 293
Db 299 NS 300
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